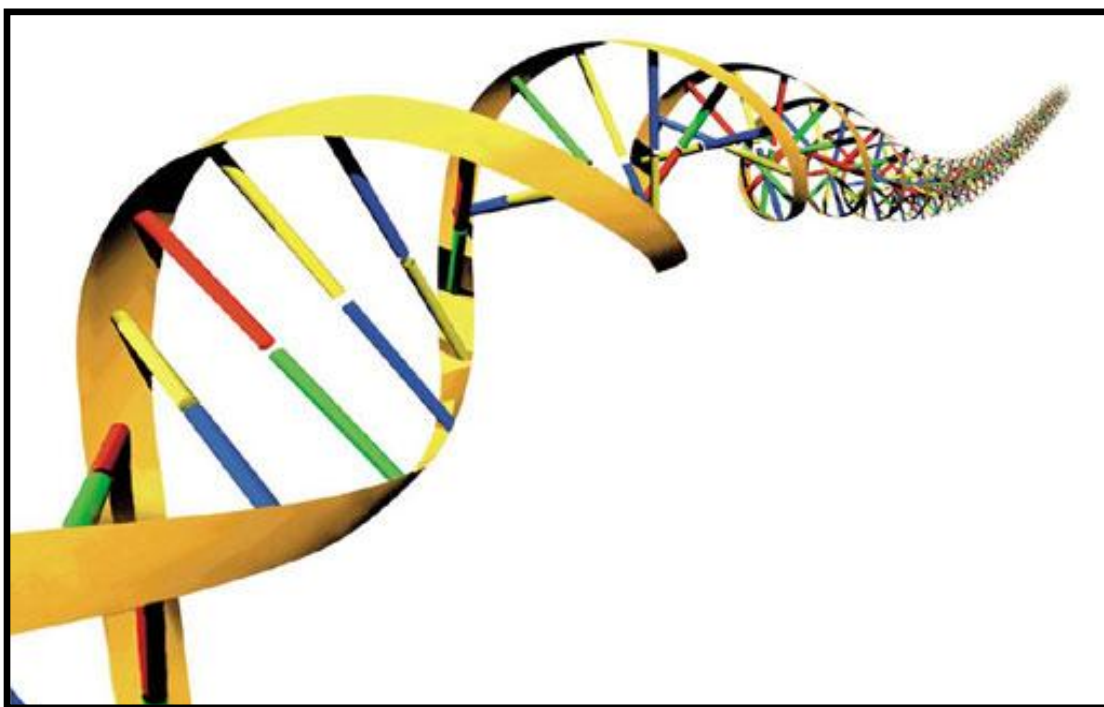


Important notes in

Molecular Biology

for first year medical students



presented by

bio  chemistry
different view

إهداء

Molecular Biology

MCQs

-1

-2

MCQs

-3

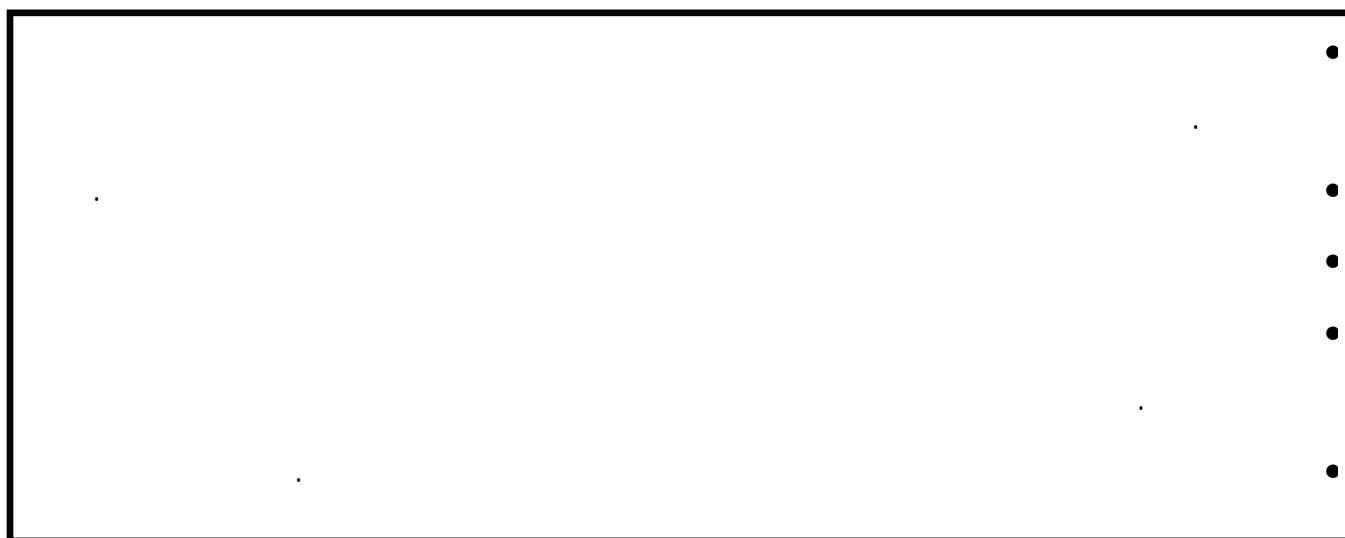
Nucleotide chemistry

- Pyrimidine bases :- uracil(in RNA), thymine(In DNA) & cytosine.
- Purine bases:- guanine & adenine
- Tautomers :-
 - 1- Adenine & cytosine form amino or imino (mostly amino).
 - 2- Guanine & thymine form keto or enol (mostly keto).
- Anti-conformation:the nucleotide & base are not in the same side to glycosidic bond.(the predominant)
- Syn-conformation: the nucleotide & base are in the same side to glycosidic bond.
- Phosphodiester bond :- 3' to 5' between two nucleotide
- Nucleoside :- nitrogenous base & pentose sugar
- Nucleotide :- nitrogenous base & pentose sugar & phosphate
- **Importance of nucleic acids :**
 - 1- DNA or RNA.
 - 2- High energy sources ,e.g. ATP.
 - 3- Coenzymes:- FAD , NAD.
 - 4- Regulatory function :- 2ry messenger cAMP .
 - 5- Activation methyl group :-s-adenosyl methionine
 - 6- Important intermediates UDP-glucose
 - 7- Synthetic analogues
 - ✓ Anti-tumor :- 5-flurouracil , 6-mercaptopurine.
 - ✓ Antiviral agent:- AZT for HIV.
 - ✓ TTT of gout :- allopurinol inhibit xanthine oxidase.

()	()	()	()

DNA structure

- DNA is polar due to it has phosphate at 5' end & (OH) 3' end.
- Chargaff rule & base complementarity (A=T) 2 H bond, (G≡C) 3 H bond.
- Waston Crick double helix model (B-form)
 - ✓ Right handed double helix
(hydrophilic deoxyribose-P outside)(hydrophobic base inside)
 - ✓ Antiparallei
 - ✓ 10 base pair per turn
 - ✓ Minor & major groove.
- Staking interaction by (hydrogen bond & hydrophobic interaction)
- Denaturation of DNA 1- Change in pH. 2- heating
- A-T base-paires is less stable than G-C
- Melting temperatureTM:- point ay which 50% of DNA molecule exists as single strand.
- Z-form :- Lt handed helix ,zigzag , 12 bp\turn
- A-form:- Rt handed helix, 11 bp\turn. Not found in nature.
- Human genome:- total DNA of chromosomes in a cell
- Histones
 - ✓ 5 different types(H1,H2A,H2B,H3,H4)
 - ✓ Rich in basic amino acids arginine & lysine
 - ✓ Nucleosome:- octamer protein(H2A,H2B,H3,H4)+DNA
 - ✓ H1 present in between nucleosome . linker coromosomes.



Replication

- Central dogma is flow of formation for DNA to RNA to protein.
- DNA replication is **semiconservative** manner.(each daughter contain parent DNA & new one.)
- Ori C** is the origin of replication in prokaryotes, **ARS** in eukaryotes (many origin of replication "AT base pair")
- Prepriming complex** composed of :-
 - Dna A protein recognize origin of replication & separate small region by ATP hydrolysis.
 - Helicase enzyme separate double helix by cleavage of hydrogen bonds.(need ATP)
 - (SSB) bind single strand prevent repriming & protect from nucleases
- Topoisomerase has nuclease & ligase activity to solve supercoils.

Topoisomerase I	Topoisomerase II
cut one strand	Cut two strands
Not need ATP	Need ATP

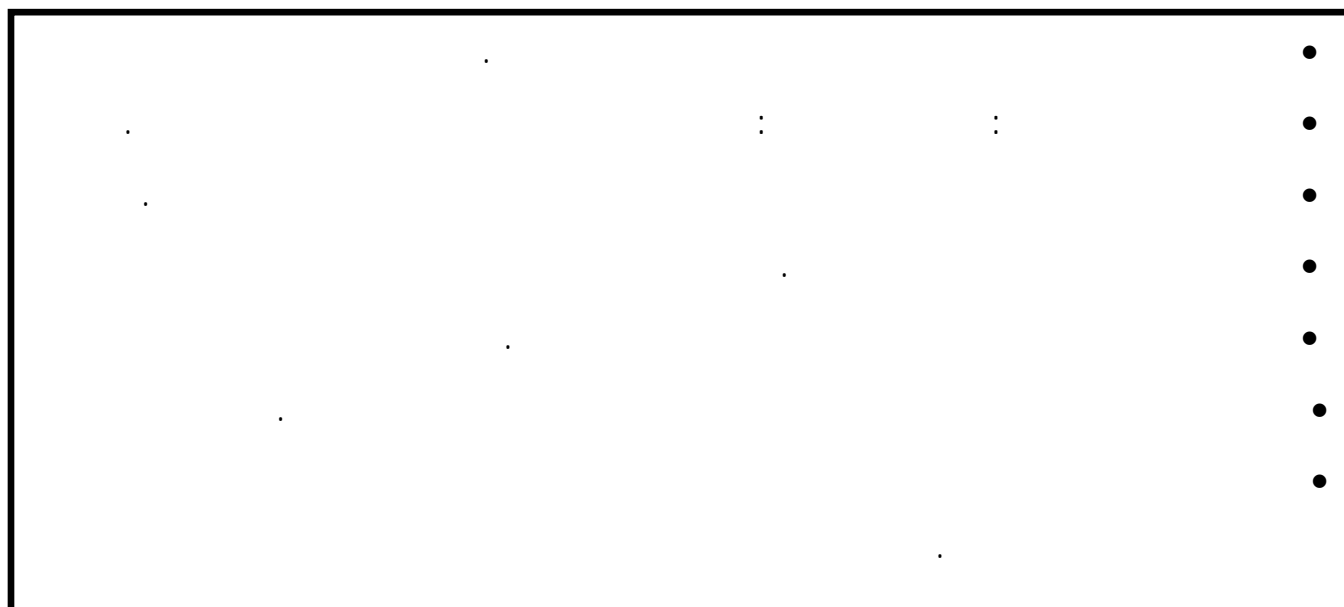
- DNA gyrase : is type II topoisomerase present in bacterio make -Ve supercoils.
- DNA replications is bidirectional.
- Polymerases
 - Cannot initiate DNA synthesis (need primer)
 - use deoxynucleoside triphosphate then release PPi
 - only from 5' to 3' (read DNA template from 3' to 5')
- primosome** complex is prepriming complex + primase.
- Leading strand is formed continuously & need one primer
(follow helicase & replication fork)
- Lagging strand dis continuously & need many primer
(opposite helicase & replication fork)
- Fragment formed in lagging strand are called Okazaki fragments.
- Polymerase I has three activities :-
 - Polymerase 5' to 3' : replace primer
 - Exonuclease from 3' to 5' : proof reading activity
 - Exonuclease from 5' to 3' : remove primer & repair (difference from 3' to 5')

Feature (prokaryotes)	Pol I	Pol II	Pol III
Exonuclease from 5' to 3'	+	--	--
Exonuclease from 3' to 5'	+	+	+
Rate of synthesis	600	30	30000
Replication	+	--	+
repair	+	?	+

- Eukaryotic replication :-
 - 1- Multiple origin
 - 2- RNase H remove primer
 - 3- occur only in S phase
 - 4- check points (cyclins)

Polymerase (eukaryotes)	function	Proof reading
Pol α	Primase & polymerase	No
Pol β	Repair	No
Pol γ	Replicate mitochondrial DNA	Yes
Pol δ	Replication	Yes
Pol ϵ	Repair	yes

- Tolemers :-DNA-protein complex at end of chromosome (to solve problem of 5' end in lagging strands)
- Tolemers is biologic clock for cell
- Tolemerase in germ , stem & cancer cells (contain reverse transcriptase & short piece of RNA).



DNA repair

- If there is no repair this cause
 - 1- Apoptosis: programmed cell death.
 - 2- Malignant tumor due to unrepaired lesion in tumor suppressor genes

A- Repair of thymine dimmer :- (formed by UV rays & prevent replication)

- Direct repair (photo reactivation):-
In bacteria visible light \rightarrow (+) photolyase \rightarrow reverse damage.
- Nucleotide-excision repair :- (mainly in human)
 - 1- UVr-ABC exinuclease :-made to cuts in DNA to remove short oligonucleotide that contain dimmer (12 in bacteria , 29 in human)
 - 2- DNA polymerase (I in bacteria , ϵ in human), DNA ligase .

B- Base excision repair : remove &repair the defective base only

- 1- DNA glycosylase : remove abnormal base to create AP site (cleaveN- glycosidic bond)
- 2- AP endonucleases : cut phosphodiester bond at 5' end of AP site
- 3- AP lyase : remove the single empty sugar phosphate
- 4- DNA polymerase I.
- 5- Ligase.

C- Methyl directed repair (mismatch repair):

Identification by Mut protein (S,H,L) to new strand (non methylated)

Endonuclease (Mut H) >> Helicase & Exonuclease >> DNA polymerase I >> Ligase.

- Hereditary nopolyposis colorectal cancer is due to mutation in proteins of mismatch repair.
- Xeroderma pigmentosum (XP): defect in nucleotide excision repair gene lead to skin cancers.

RNA structure

- RNA are destroyed by alkali & contain intrastrand H-bonds,
 - but DNA is resistant & contain H-bonds between two strands.
- 1- m RNA (messenger) 5% of the total RNA
 - exons :- coding regions
 - Introns:- untranslated region in-between exons
 - untranslated region in both 5' & 3' end (UTRs) regulatory regions
 - 5' end is 7-methylguanosine cap
 - 3' end contain poly A tail.
 - 2- r RNA (ribosomal) 80 % of total RNA
 - @ prokaryotes (23S , 16S , 5S) @ eukaryotes (28S , 18S , 5.8S , 5S)
 - 3- t RNA (transfer) adaptors (contain anticodon) 15% of total RNA
 - has CCA at 3' end (amino acids binding site)
 - has 4 single stranded loops
 - has modified bases.
 - Contain intra-chain H-bonds (cloverleaf shape).

Transcription

- Template strand (antisense) :- the strand that will be transcribed
- Coding strand (sense):- the other strand
- Promoter :-
 - 1- Specific sequence on DNA that recognized to initiate RNA synthesis at specific point
 - 2- Upstream to the template strand, near the gene that will be transcribed.
- Prokaryotic RNA polymerase:- (holoenzyme)
 - 1- Core enzyme : 4 subunit (2 α , 1 β , 1 β') responsible for 5' to 3' polymerase activity
 - 2- The σ sigma subunit :- recognize promoter region
 - 3- Ω ohm subunit :- unclear function.
- Eukaryotic RNA polymerase :

name	Product
RNA POL I	Larger ribosomal RNA (28S, 18S, 5.8S)
RNA POL II	mRNA & snRNA
RNA POL III	tRNA & small ribosomal RNA (5S)

- **Initiation in prokaryotes:-**
 - ✓ Pinbow box or TATA box :- (-10), TATAAT, absolutely essential for transcription
 - ✓ TG box :- (-35), TTGACA, allow very high transcription rate .
 - ✓ Closed complex :- holoenzyme + double strand DNA.
- **Initiation in eukaryotes:-**
 - ✓ Basal eukaryotic transcription complex :- RNA polymerase + transcription factor.
 - ✓ Hogness box :- TATAAA, bind to transcription factor (promoter).
 - ✓ CAAT box :- CACGGTG, regulatory sequences.
- **Regulation of transcription in eukaryotes**
 - 1- **Chromosomal remodeling**
 - a- Histone acetylation\deacetylation:-*
Acetylation of lysine in histones eliminate +ve charge & decrease interaction with DNA.
Acetylation made by histone acetyltransferase, & removed by deacetylases
 - b- DNA methylation :-*
Methylation of cytosine residues in 5-carbon position
Prevent binding of transcription factors to promoter
Made by methyl transferase
Methylation induce histone deacetylation
 - 2- **Cis-acting element (DNA sequences)**
 - a- Silencers :- bind with repressor to decrease rate of transcription.
 - b- Enhancers:- bind to factors to increase rate of transcription.
 - 3- **Trans acting elements (regulatory proteins)**
 - a- Repressor :- bind with silencer to decrease rate of transcription
 - b - Inducer :- bind with repressor to detach it & increase rate of transcription.

- Open complex: - holoenzyme + single strand DNA.
- Elongation cannot proceed until sigma factor dissociate from enzyme.
- Most transcripts originate using purine nucleotide triphosphate (GTP & ATP).
- **Termination in prokaryotes:-**
 - 1- **Rho -independent termination (intrinsic factor):-**
 - ✓ Loop structure (palindromic sequence rich in G-C inverted repeated)
 - ✓ Poly A sequence (due to repeated T in DNA).
 - 2- **Rho -dependent termination :-**
 - ✓ ATP dependent.
 - ✓ Need Rho protein.
- Post transcription modification :-
 - 1- rRNA form subunits
 - 2- tRNA processing (cleave the original transcript by ribonucleases)
 - ✓ remove introns
 - ✓ add CCA to 3' terminal
 - ✓ modification of some bases
 - 3- mRNA
 - ✓ heterogenous nuclear RNA:- precursor of mRNA.
 - ✓ 5' capping
 - ✓ Addition of poly A tail,by polyadenylate polymerase,use ATP as a substrate.
 - ✓ Remove introns(splicing) by (snRNA &protein)(snRNP)
 - ✓ Systemic lupus erythromatosis due to autoimmune response toward snRNP.
 - ✓ Alternative slicing produce proteins with different activity e.g. tropomyosin ,lgs
- Reverse transcriptase :- produce DNA from RNA
(In prokaryotes ,e.g. HIV) (in eukaryotes e.g. telomerase)
- Ribonuclease H digest RNA strand
- integrase enzyme introduce complementary DNA into human cells

عن عبد الله بن مسعود رضي الله عنه قال:
 سألت النبي صلى الله عليه وسلم أي العمل أحب إلى الله عز وجل؟
 قال: (الصلاة على وقتها)
 قال: ثم أي؟
 قال: (بر الوالدين)
 قال: ثم أي؟
 قال: (الجهاد في سبيل الله)

Genetic code

- Nonsense codons (termination codons) are tree in number, start codon only one.
- Degeneracy :- multiple codons decode the same amino acid (usually change is in the third base)
- Degeneracy decrease possibility of additional of abnormal AA with mutation in third base.
- Wobble hypothesis:-mechanism allow one tRNA to recognize more than one codon for AA.
- Unambiguous: code is specific (code fore one AA only).
- Neither overlapping nor punctuation in mRNA.
- Universal : all organisms use the same codes (with some exeptions)
- Mutation :


	A- Point mutation	B- Frame shift mutation
definition	Alter one base only	Add or delete one or two nucleotide
Types	Transition :-from purine to purine or pyrimidine to pyrimidine. Transversion :-from purine to pyrimidine & vise versa	
effect	1-Silent mutation (no effect,same amino acid) 2- Missense (other amino acid) (acceptable,partial or not) 3- Nonsense (termination code)	1- Premature termination 2- Altering the reading frame

- Cystic fibrosis(CF)
 - ✓ Affect lung & digestive system
 - ✓ Deletion of three nucleutides (for phenylalanine),prevent normal folding of CF transmembrane regulator (CFTR)
 - ✓ CFTR normally function as CL channel in epithelium
- Huntington disease
 - ✓ Amplification of CAG (glutamine) in Huntington protein.
 - ✓ Become unstable & accumulate cause neurodegenerative disorders
- Splice site mutation (e.g. β -thalassemia)

Translation

- If one amino acid is missed , transalation stops at the codon of this amino acids.
- Charged († RNA) :- † RNA covalently attached to amino acid.(amino acid is activated).
- Codon & anticodon are complementary & anti parallel.
- Aminoacyl - † RNA synthetase :
 - 1- amino acid + ATP → aminoacyl-AMP + PP_i
 - 2- aminoacyl-AMP + tRNA → aminoacyl-tRNA + AMP
- ✓ 20 different Aminoacyl - † RNA synthetase present (one for each amino acid).
- ✓ Highly specific has proofreading activity .
- ✓ The formation of one Aminoacyl - † RNA needs 2 high energy phosphate bonds.
- Ribose (large & small unit)
 - ✓ Prokaryotes (50S & 30S)(together 70S) ----- Eukaryotes (60S & 40S)(together 80).
 - 1- **A site** : bind to amino acyl-† RNA .
 - 2- **P site** : contain peptidyl † RNA .
 - 3- **E site** : empty † RNA to exit.
 - ✓ Types
 - 1- Free ribosome :- synthesize proteins present in cell
 - 2- Membrane bounded ribosomes :- synthesize proteins that will be secreted or present in lysosome or gogi membrane .
 - 3- Polysomes :-intensive protein synthesis (several ribosome translate one mRNA)
- Transalation synthesize protein from amino terminal to carboxyl terminal .
- Polycistronic (prokaryotic m RNA contain several coding region)
- Monocistronic(eukaryotic m RNA contain one coding region).
- Difference in initiation between eukaryotes & prokaryotes :

Aspect	eukaryotes	prokaryotes
Binding of m RNA to small ribosomal subunit	Cap at 5' end of mRNA binds eIFs and 40S containing tRNA ^{met} , mRNA is scanned for AUG start codon	Shine-Dalgarno sequence upstream to AUG bind to small ribosomal unit (16S)
First amino acid	methionine	Formyl-methionine
Initiation factors	eIFs(12 or more)	IFs (3)

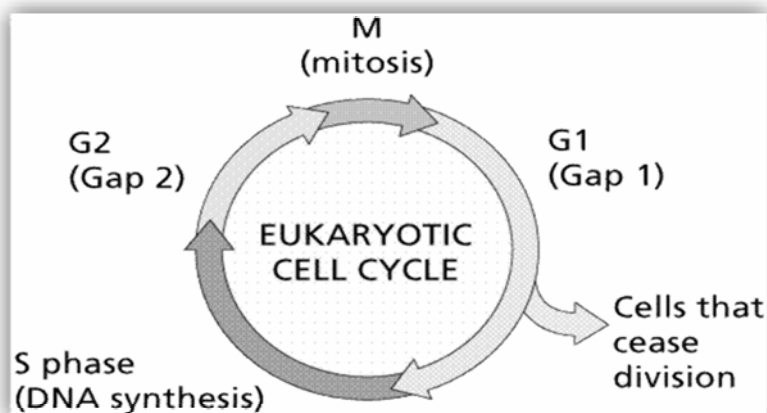
- 

Post translation

- Protein folding occurs co-translationally .
- Any mutation of any amino acid result in problems in folding
- Folding occur to make hydrophobic amino acids inside protein & hydrophilic amino acids in the surface.
- **Chaperones** :- (protect the protein from misfolding)
 - 1- De novo protein folding
 - 2- Stabilize proteins under stress (high temperature)(classified as heat shock protein)
 - 3- Maintain polypeptide chain in a loosely manner for translocation across organelles.
- **Misfolding**
 - 1- **Alzheimer disease**
 - ✓ Accumulation of misfolded protein called amyloid precursor protein(APP)
 - ✓ APP is degraded to form beta-amyloid that form plaques around neurons.
 - ✓ Loss of connection between nerve cells & brain
 - 2- **Prion disease**
 - ✓ Occur in human & animals
 - ✓ Create microscopic spong like holes in brain
 - 3- **Alpha 1 antitrypsin deficiency**
 - ✓ Accumulation in lung & liver
 - ✓ Elastase will destroy lung tissue & decrease elasticity
 - ✓ Cause emphysema in lung.
- **Post translation modification of polypeptide chains**
 - a- Trimming :-remove part by endoproteases to make protein active. E.g. (insulin & zymogens)
 - b- Covalent alteration
 - 1- Phosphorylation :-in (OH) of amino acids in enzymes to increase or decrease activity.
 - 2- Glycosylation :- in (OH) of amino acids & amide occur in golgi &(ER) to target protein.
 - 3- hydroxylation :- proline & lysine in collagen
(for maximizing interchain H bonds & stabilizing triple helical structure)
- **Protein degradation** :- by ubiquitin made isopeptide bond by carboxyl of it & epsilon amino in lysine to be degraded in proteosome.

important notes in MCQs

- Adenosine is the nucleoside of adenine
- Adenylic acid is the nucleotide of adenine (adenosine phosphate)
- The sugar of DNA is 5'-deoxyribose, sugar of RNA is ribose
- DNA strand is not branched.
- Denaturation of DNA (melting) (heating) disrupts hydrogen bonds.
- Denaturation increase DNA absorbance at 260 nm.
- RNA is not absolutely single strand (tRNA contain double strands)
- Okazaki fragments are not in leading strand (only in lagging).
- mRNA has the greatest sequence diversity between RNAs in cell
- retroviruses have reverse transcriptase
- the cap in mRNA is important to protect from nuclease & initiation of translation.
- Post transcription modification in which there is added sequence (mRNA & tRNA)
- Amino acid binds to CCA of tRNA by ester bond.
- Activator is the factor that control initiation of transcription.
- Non sense codon are not identical in nucleus & mitochondria.
- in polysome ,ribosome synthesizes the longest peptide chain is the nearest to 3'end of mRNA.
- Translocation in translation need EF & GTP



تصحيح بعض الإجابات الخاطئة في كتاب القسم

Chapter 4	1 (d)					
Chapter 5	11 (all except زود على السؤال)	32 (b)				
Chapter 7	5 (b)	6 (e)	7 (c)	8 (b)	9 (a)	10 (d)

bio chemistry

different view

- Complete course in biochemistry for first year medical students.
- You can easily understand and study biochemistry.



: bio_differentview@hotmail.com

لمزيد من الإستفسارات
سنتر المستقبل : 10 ش مستشفى الدمرداش ت / 0166714987